

7. SEQUENCE LISTING

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symersky, Jindrich

(ii) TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold, White & Durkee
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(E) COUNTRY: U.S.
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/017,678
(B) FILING DATE: 16-MAY-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: TAMK:193

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATAACATCTG GGAATAAATC AACGAATGTT ACGGTTTCATA AAAGTGAAGC GGGAACAAGT 60
AGTGTTTTCT ATTATAAAAC GGGAGATATG CTACCAGAAG ATACGACACA TGTACGATGG 120
TTTTTAAATA TTAACAATGA AAAAAGTTAT GTATCGAAAG ATATTACTAT AAAGGATCAG 180
ATTCAAGGTG GACAGCAGTT AGATTTAAGC ACATTAAACA TTAATGTGAC AGGTACACAT 240
AGCAATTATT ATAGTGGACA AAGTGCAATT ACTGATTTTG AAAAAGCCTT TCCAGGTTCT 300
AAAATAACTG TTGATAATAC GAAGAACACA ATTGATGTAA CAATTCCACA AGGCTATGGG 360
TCATATAATA GTTTTCAAT TAACTACAAA ACCAAAATTA CGAATGAACA GCAAAAAGAG 420
TTTGTTAATA ATTCACAAGC T 441

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Gly Ser His His His His His His Gly Ser Ile Thr Ser Gly
1 5 10 15
Asn Lys Ser Thr Asn Val Thr Val His Lys Ser Glu Ala Gly Thr Ser
20 25 30
Ser Val Phe Tyr Tyr Lys Thr Gly Asp Met Leu Pro Glu Asp Thr Thr
35 40 45
His Val Arg Trp Phe Leu Asn Ile Asn Asn Glu Lys Ser Tyr Val Ser
50 55 60
Lys Asp Ile Thr Ile Lys Asp Gln Ile Gln Gly Gly Gln Gln Leu Asp
65 70 75 80
Leu Ser Thr Leu Asn Ile Asn Val Thr Gly Thr His Ser Asn Tyr Tyr
85 90 95

Ser Gly Gln Ser Ala Ile Thr Asp Phe Glu Lys Ala Phe Pro Gly Ser
100 105 110

Lys Ile Thr Val Asp Asn Thr Lys Asn Thr Ile Asp Val Thr Ile Pro
115 120 125

Gln Gly Tyr Gly Ser Tyr Asn Ser Phe Ser Ile Asn Tyr Lys Thr Lys
130 135 140

Ile Thr Asn Glu Gln Gln Lys Glu Phe Val Asn Asn Ser Gln Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACGATAAAA ATGGAAAAAT ACAAATGGT GACATGATTA AAGTGGCATG GCCGACAAGC	60
GGTACAGTAA AGATAGAGGG TTATAGTAAA ACAGTACCAT TAACTGTTAA AGGTGAACAG	120
GTGGGTCAAG CAGTTATTAC ACCAGACGGT GCAACAATTA CATTCAATGA TAAAGTAGAA	180
AAATTAAGTG ATGTTTCGGG ATTTGCAGAA TTTGAAGTAC AAGGAAGAAA TTTAACGCAA	240
ACAAATACTT CAGATGACAA AGTAGCTACG ATAACATCTG GGAATAAATC AACGAATGTT	300
ACGGTTCATA AAAGTGAAGC GGAACAAGT AGTGTTTTCT ATTATAAAC GGGAGATATG	360
CTACCAGAAG ATACGACACA TGTACGATGG TTTTAAATA TTAACAATGA AAAAAATTAT	420
GTATCGAAAG ATATTACTAT AAAGGATCAG ATTCAAGGTG GACAGCAGTT AGATTTAAGC	480
ACATTAAACA TTAATGTGAC AGGTACACAT AGCAATTATT ATAGTGGACA AAGTGCAATT	540
ACTGATTTTG AAAAAGCCTT TCCAGGTTCT AAAATAACTG TTGATAATAC GAAGAACACA	600
ATTGATGTAA CAATTCCACA AGGCTATGGG TCATATAATA GTTTTCAAT TAACTACAAA	660
ACCAAATTA CGAATGAACA GCAAAAAGAG TTTGTTAATA ATTCACAAGC TTGGTATCAA	720
GAGCATGGTA AGGAAGAAGT GAACGGGAAA TCATTTAATC ATACTGTGCA CAATATTAAT	780
GCTAATGCCG GTATTGAAGG TACTGTAAAA GGTGAATTAA AAGTTTTAAA ACAGGATAAA	840
GATACCAAG	849

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Lys Val
1 5 10 15

Ala Thr Ile Thr Ser Gly Asn Lys Ser Thr Asn Val Thr Val His Lys
20 25 30

Ser Glu Ala Gly Thr Ser Ser Val Phe Tyr Tyr Lys Thr Gly Asp Met
35 40 45

Leu Pro Glu Asp Thr Thr His Val Arg Trp Phe Leu Asn Ile Asn Asn
50 55 60

Glu Lys Ser Tyr Val Ser Lys Asp Ile Thr Ile Lys Asp Gln Ile Gln
65 70 75 80

Gly Gly Gln Gln Leu Asp Leu Ser Thr Leu Asn Ile Asn Val Thr Gly
85 90 95

Thr His Ser Asn Tyr Tyr Ser Gly Gln Ser Ala Ile Thr Asp Phe Glu
100 105 110

Lys Ala Phe Pro Gly Ser Lys Ile Thr Val Asp Asn Thr Lys Asn Thr
115 120 125

Ile Asp Val Thr Ile Pro Gln Gly Tyr Gly Ser Tyr Asn Ser Phe Ser
130 135 140

Ile Asn Tyr Lys Thr Lys Ile Thr Asn Glu Gln Gln Lys Glu Phe Val
145 150 155 160

Asn Asn Ser Gln Ala Trp Tyr Gln Glu His Gly Lys Glu Glu Val Asn
165 170 175

Gly Lys Ser Phe Asn His Thr Val His Asn Ile Asn Ala Asn Ala Gly
180 185 190

Ile Glu Gly Thr Val Lys Gly Glu Leu Lys Val Leu Lys Gln Asp Lys
195 200 205

Asp Thr Lys
210

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCACGAGATA TTTCATCAAC GAATGTTACA GATTTAACTG TATCACCGTC TAAGATAGAA	60
GATGGTGGTA AAACGACAGT AAAAATGACG TTCGACGATA AAAATGGAAA AATACAAAAT	120
GGTGACATGA TTAAAGTGGC ATGGCCGACA AGCGGTACAG TAAAGATAGA GGGTTATAGT	180
AAAACAGTAC CATTAACTGT TAAAGGTGAA CAGGTGGGTC AAGCAGTTAT TACACCAGAC	240
GGTGCAACAA TTACATTCAA TGATAAAGTA GAAAAATTAA GTGATGTTTC GGGATTTGCA	300
GAATTTGAAG TACAAGGAAG AAATTTAACG CAAACAAATA CTTCAGATGA CAAAGTAGCT	360
ACGATAACAT CTGGGAATAA ATCAACGAAT GTTACGGTTC ATAAAAGTGA AGCGGGAACA	420
AGTAGTGTTT TCTATTATAA AACGGGAGAT ATGCTACCAG AAGATACGAC ACATGTACGA	480
TGGTTTTTTAA ATATTAACAA TGAAAAAAGT TATGTATCGA AAGATATTAC TATAAAGGAT	540
CAGATTCAAG GTGGACAGCA GTTAGATTTA AGCACATTAA ACATTAATGT GACAGGTACA	600
CATAGCAATT ATTATAGTGG ACAAAGTGCA ATTACTGATT TTGAAAAAGC CTTTCCAGGT	660
TCTAAAATAA CTGTTGATAA TACGAAGAAC ACAATTGATG TAACAATTCC ACAAGGCTAT	720
GGGTCATATA ATAGTTTTTC AATTAAC TAC	780
GAGTTTGTTA ATAATTCACA AGCTTGGTAT CAAGAGCATG GTAAGGAAGA AGTGAACGGG	840
AAATCATTTA ATCATACTGT GCACAATATT AATGCTAATG CCGGTATTGA AGGTACTGTA	900
AAAGGTGAAT TAAAAGTTTT AAAACAGGAT AAAGATACCA AGGCTCCTAT AGCTAATGTA	960
AAATTTAAAC TTTCTAAAAA AGATGGATCA GTTGTAAGG ACAATCAAAA AGAAATTGAG	1020
ATTATAACAG ATGCAAACGG TATTGCTAAT ATTAAAGCGT TGCCTAGTGG AGACTATATT	1080
TTAAAAGAAA TAGAGGCGCC ACGACCGTAT ACATTTGATA AGGATAAAGA ATATCCGTTT	1140
ACTATGAAAG ATACAGATAA TCAGGGATAT TTTACGACTA TTGAAAATGC AAAAGCGATA	1200
GAAAAACAA AAGATGTTTC TGCTCAAAG GTTTGGGAAG GCACTCAAAA AGTGAAACCA	1260

ACGATTTATT TCAAGTTGTA CAAACAAGAT GACAATCAAA ATACAACACC AGTAGACAAA 1320
 GCAGAGATTA AAAAATTAGA AGATGGAACG ACAAAGTGA CATGGTCTAA TCTTCCGGAA 1380
 AATGACAAAA ATGGCAAGGC TATTAAATAT TTAGTTAAAG AAGTAAATGC TCAAGGTGAA 1440
 GATACAACAC CAGAAGGATA TACTAAAAAA GAAAATGGTT TAGTGGTTAC TAATACTGAA 1500

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Arg	Gly	Ser	His	His	His	His	His	Gly	Ser	Ala	Arg	Asp	Ile	1	5	10	15	
Ser	Ser	Thr	Asn	Val	Thr	Asp	Leu	Thr	Val	Ser	Pro	Ser	Lys	Ile	Glu	20	25	30	
Asp	Gly	Gly	Lys	Thr	Thr	Val	Lys	Met	Thr	Phe	Asp	Asp	Lys	Asn	Gly	35	40	45	
Lys	Ile	Gln	Asn	Gly	Asp	Met	Ile	Lys	Val	Ala	Trp	Pro	Thr	Ser	Gly	50	55	60	
Thr	Val	Lys	Ile	Glu	Gly	Tyr	Ser	Lys	Thr	Val	Pro	Leu	Thr	Val	Lys	65	70	75	80
Gly	Glu	Gln	Val	Gly	Gln	Ala	Val	Ile	Thr	Pro	Asp	Gly	Ala	Thr	Ile	85	90	95	
Thr	Phe	Asn	Asp	Lys	Val	Glu	Lys	Leu	Ser	Asp	Val	Ser	Gly	Phe	Ala	100	105	110	
Glu	Phe	Glu	Val	Gln	Gly	Arg	Asn	Leu	Thr	Gln	Thr	Asn	Thr	Ser	Asp	115	120	125	
Asp	Lys	Val	Ala	Thr	Ile	Thr	Ser	Gly	Asn	Lys	Ser	Thr	Asn	Val	Thr	130	135	140	
Val	His	Lys	Ser	Glu	Ala	Gly	Thr	Ser	Ser	Val	Phe	Tyr	Tyr	Lys	Thr	145	150	155	160
Gly	Asp	Met	Leu	Pro	Glu	Asp	Thr	Thr	His	Val	Arg	Trp	Phe	Leu	Asn	165	170	175	
Ile	Asn	Asn	Glu	Lys	Ser	Tyr	Val	Ser	Lys	Asp	Ile	Thr	Ile	Lys	Asp				

180										185					190						
Gln	Ile	Gln	Gly	Gly	Gln	Gln	Leu	Asp	Leu	Ser	Thr	Leu	Asn	Ile	Asn						
		195					200					205									
Val	Thr	Gly	Thr	His	Ser	Asn	Tyr	Tyr	Ser	Gly	Gln	Ser	Ala	Ile	Thr						
	210					215					220										
Asp	Phe	Glu	Lys	Ala	Phe	Pro	Gly	Ser	Lys	Ile	Thr	Val	Asp	Asn	Thr						
225					230					235					240						
Lys	Asn	Thr	Ile	Asp	Val	Thr	Ile	Pro	Gln	Gly	Tyr	Gly	Ser	Tyr	Asn						
				245					250					255							
Ser	Phe	Ser	Ile	Asn	Tyr	Lys	Thr	Lys	Ile	Thr	Asn	Glu	Gln	Gln	Lys						
			260					265					270								
Glu	Phe	Val	Asn	Asn	Ser	Gln	Ala	Trp	Tyr	Gln	Glu	His	Gly	Lys	Glu						
		275					280					285									
Glu	Val	Asn	Gly	Lys	Ser	Phe	Asn	His	Thr	Val	His	Asn	Ile	Asn	Ala						
	290					295					300										
Asn	Ala	Gly	Ile	Glu	Gly	Thr	Val	Lys	Gly	Glu	Leu	Lys	Val	Leu	Lys						
305					310					315					320						
Gln	Asp	Lys	Asp	Thr	Lys	Ala	Pro	Ile	Ala	Asn	Val	Lys	Phe	Lys	Leu						
				325					330					335							
Ser	Lys	Lys	Asp	Gly	Ser	Val	Val	Lys	Asp	Asn	Gln	Lys	Glu	Ile	Glu						
			340					345					350								
Ile	Ile	Thr	Asp	Ala	Asn	Gly	Ile	Ala	Asn	Ile	Lys	Ala	Leu	Pro	Ser						
	355					360						365									
Gly	Asp	Tyr	Ile	Leu	Lys	Glu	Ile	Glu	Ala	Pro	Arg	Pro	Tyr	Thr	Phe						
	370					375					380										
Asp	Lys	Asp	Lys	Glu	Tyr	Pro	Phe	Thr	Met	Lys	Asp	Thr	Asp	Asn	Gln						
385					390					395					400						
Gly	Tyr	Phe	Thr	Thr	Ile	Glu	Asn	Ala	Lys	Ala	Ile	Glu	Lys	Thr	Lys						
				405					410					415							
Asp	Val	Ser	Ala	Gln	Lys	Val	Trp	Glu	Gly	Thr	Gln	Lys	Val	Lys	Pro						
			420					425					430								
Thr	Ile	Tyr	Phe	Lys	Leu	Tyr	Lys	Gln	Asp	Asp	Asn	Gln	Asn	Thr	Thr						
	435						440					445									
Pro	Val	Asp	Lys	Ala	Glu	Ile	Lys	Lys	Leu	Glu	Asp	Gly	Thr	Thr	Lys						
	450					455					460										

Val Thr Trp Ser Asn Leu Pro Glu Asn Asp Lys Asn Gly Lys Ala Ile
 465 470 475 480

Lys Tyr Leu Val Lys Glu Val Asn Ala Gln Gly Glu Asp Thr Thr Pro
 485 490 495

Glu Gly Tyr Thr Lys Lys Glu Asn Gly Leu Val Val Thr Asn Thr Glu
 500 505 510 -

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Arg Gly Ser His His His His His His Gly Ser Met Val Ala Ala
 1 5 10 15

Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val
 20 25 30

Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly
 35 40 45

Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys
 50 55 60

Gly Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly
 65 70 75 80

Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val
 85 90 95

Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe
 100 105 110

Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met
 115 120 125

Pro Ala Tyr Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr
 130 135 140

Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val
 145 150 155 160

Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile Lys Gly Thr
 165 170 175

Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr
 180 185 190
 Val Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn
 195 200 205
 Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr
 210 215 220
 Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser
 225 230 235 240
 Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn
 245 250 255
 Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro
 260 265 270
 Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile
 275 280 285
 Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly
 290 295 300
 Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val
 305 310 315 320
 Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val
 325 330 335
 Val Pro Glu Gln Pro Asp Glu Gln Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Gly Ser His His His His His His Gly Ser Glu Gly Gly Gln
 1 5 10 15
 Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro
 20 25 30
 Lys Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val
 35 40 45

Pro	Gln	Ile	His	Gly	Gln	Asn	Lys	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp
50						55					60				
Thr	Glu	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	His	Gly	Gly	Asn	Ile	Ile	Asp
65					70					75				80	
Ile	Asp	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn	Lys	His	Thr
				85					90					95	-
Glu	Ile	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Ser	Tyr	Gln	Phe
			100					105						110	
Gly	Gly	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu	Pro	Lys	Val
		115					120					125			
Ser	Gly	Gln	Asn	Glu	Phe	Asp	Ile	Lys	Leu	Asn					
130						135									

All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the composition, methods and in the steps or in the sequence of steps—of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims. Accordingly, the exclusive rights sought to be patented are as described in the claims.